

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:42:51 ; Search time 1988 Seconds
(without alignments)
585.827 Million cell updates/sec

Title: US-09-435-471B-9

Perfect score: 39

Sequence: 1 taactctgaatttttaaaacccgaagtcagagctagta 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 203984

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	45.6	46	9	AA875851 OB34C05.S
2	17.4	44.6	56	29	CL002662 CL002662 02S0169.0
3	17.2	44.1	50	28	BZ765559 SALK_1316
4	17	43.6	56	28	B02877 B02877 CSRL-161G3-

C	5	16.8	43.1	45	28	BZ766643	BZ766643 SALK_1376
C	6	16.6	42.6	51	13	BQ625561	BQ625561 rd17c06.Y
C	7	16.6	42.6	54	29	DME545095	AJ545095 Drosophila
C	8	16.4	42.1	53	29	CL002273	CL002273 02S0105-0
C	9	16.4	42.1	60	28	BZ665081	BZ665081 SALK_1106
C	10	16.2	41.5	55	28	BZ662725	BZ662725 SALK_0262
C	11	16.2	41.5	57	14	CA334810	CA334810 NISC_1c01
C	12	16	41.0	50	9	AU106257	AU106257 AU106257
C	13	15.8	40.5	51	13	BQ786274	BQ786274 sag65h01.
C	14	15.8	40.5	52	9	AA531325	AA531325 nj51g04.s
C	15	15.8	40.5	59	14	W38842	W38842 zb28c08.r1
C	16	15.6	40.0	34	28	BZ764154	BZ764154 SALK_1240
C	17	15.6	40.0	34	28	BZ764155	BZ764155 SALK_1240
C	18	15.6	40.0	56	10	AW510712	AW510712 hd36e09.x
C	19	15.4	39.5	60	28	BZ761908	BZ761908 SALK_0830
C	20	15.2	39.0	37	28	BH791558	BH791558 SALK_0604
C	21	15.2	39.0	55	28	AZ514607	AZ514607 1M0361K23
C	22	15.2	39.0	57	28	AZ537462	AZ537462 AST-2P046
C	23	15.2	39.0	60	13	BQ785544	BQ785544 saq79e10.
C	24	15	38.5	36	29	BX656784	BX656784 Arabidops
C	25	15	38.5	45	10	BE896253	BE896253 601438976
C	26	15	38.5	54	12	BI865787	BI865787 ft27e04.x
C	27	15	38.5	58	29	AL952767	AL952767 Arabidops
C	28	15	38.5	59	9	AF090227	AF090227 AF090227
C	29	15	38.5	59	9	AV561680	AV561680 AV561680
C	30	15	38.5	60	14	CF330014	CF330014 NAACL--05-
C	31	14.8	37.9	45	28	AZ812554	AZ812554 2M0079K15
C	32	14.8	37.9	45	28	BZ290823	BZ290823 SALK_0915
C	33	14.8	37.9	52	10	BF647818	BF647818 NF012D01E
C	34	14.8	37.9	58	9	AV969325	AV969325 AV969325
C	35	14.8	37.9	59	12	BG361064	BG361064 gb45d09.Y
C	36	14.6	37.4	39	28	AZ321053	AZ321053 1M0041G24
C	37	14.6	37.4	46	9	AU256186	AU256186 AU256186
C	38	14.6	37.4	50	28	BH906653	BH906653 SALK_0351
C	39	14.6	37.4	51	14	CB058336	CB058336 NISC_jx03
C	40	14.6	37.4	52	9	AA170232	AA170232 ms80g10.r
C	41	14.6	37.4	53	28	AZ488804	AZ488804 1M0319H15
C	42	14.6	37.4	60	9	AA554929	AA554929 nk31g05.s
C	43	14.6	37.4	60	12	BG271466	BG271466 nai57d04.
C	44	14.6	37.4	60	12	BG271507	BG271507 nai58b05.
C	45	14.6	37.4	60	12	BG370294	BG370294 nai29h04.

ALIGNMENTS

RESULT 1
AA875851/c 46 bp mRNA linear EST 25-MAR-1998
LOCUS ob34c05.s1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1325576 3'
DEFINITION similar to SW:AF11_HUMAN P55008 ALLOGRAFT INFLAMMATORY FACTOR-1 ;
mRNA sequence.

ACCESSION AA875851 GI:2985210
VERSION AA875851.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 46)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the T.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1..46

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1325576"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/clone_lib="NCI CGAP Kids"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGAGAGATTGGCGGCGGCAATATTTTATTTTATTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match

45.6%; Score 17.8; DB 9; Length 46;

Best Local Similarity 75.9%; Pred. No. 1.5e+04;

Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY

5 TCTGAATTTTAAACCCGAAGTCAAGAG 33

Db

39 TCGAATTTTAAAGCCCAACGAAAGAG 11

RESULT 2

CL002662/c

LOCUS CL002662 56 bp DNA linear GSS 19-DEC-2003

DEFINITION 02S0169-07A1-G05 UniformMu MutAIL Library Zea mays genomic clone

02S0169-07A1-G05, genomic survey sequence.

ACCESSION CL002662

VERSION CL002662.1 GI:40219741

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 56)

Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.

Sequence tagged transposon insertions from the UniformMu maize population

Unpublished (2003)

Contact: Donald R. McCarty

Plant Molecular and Cellular Biology Program

University of Florida

PO 110690 Gainesville, FL 32611-0690, USA

Tel: 352-392-1928 x322

Email: drmc@ufl.edu

Sequence flanking probable Mu insertion site in UniformMu line:

02S0169-07, Primer set: A

Class: transposon insertion site.

Location/Qualifiers

source

1..56

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="W22 (ACR, bz1-m9)"

/cultivar="UniformMu"

/db_xref="taxon:4577"

/clone="02S0169-07A1-G05"

/clone_lib="UniformMu MutAIL Library"

/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary

ORIGIN

primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."

Query Match

44.6%; Score 17.4; DB 29; Length 56;

Best Local Similarity 77.8%; Pred. No. 2.2e+04;

Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

5 TCTGAATTTTAAACCCGAAGTCAAG 31

Db

55 TCGAATTTCTGAACCTGATGTAAG 29

RESULT 3

BZ765559/c

LOCUS BZ765559 50 bp DNA linear GSS 13-MAR-2003

DEFINITION SALK_131696.45.85.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_131696.45.85.x, genomic survey sequence.

ACCESSION BZ765559

VERSION BZ765559.1 GI:28938112

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 50)

Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shin, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

source

1..50

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_131696.45.85.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

44.1%; Score 17.2; DB 28; Length 50;

Best Local Similarity 65.8%; Pred. No. 2.6e+04;

Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY

2 AACTGGAATTTTAAACCCGAAGTCAAGCTAGTA 39

Db

50 AATTGGAATTTTAAACCTTAAGATAAGAGAATA 13

RESULT 4

B02877/c

LOCUS B02877 56 bp DNA linear GSS 13-JUL-1996

DEFINITION CSRL-161G3-u CSRL flow sorted Chromosome 11 specific cosmid Homo

sapiens genomic clone cSRL-161G3, genomic survey sequence.

ACCESSION B02877
VERSION B02877.1 GI:1412155
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 56)
Evans, G.A., Butbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S., Harris, J., Deford, J., McFarland, J., Burzinski, K., Khan, M., Kupfer, K. and Garner, H.R.
Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)

TITLE JOURNAL
COMMENT Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
Email: gevas@utsw.swmed.edu, shane@mcdermott.swmed.edu
Seq Primer: T7
Class: cosmid ends
High quality sequence stop: 56.

FEATURES
source
1..56
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="cSRL-161G3"
/sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
/clone_lib="cSRL flow sorted Chromosome 11 specific cosmid"
/note="Vector: sCos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"

ORIGIN

Query Match 43.6%; Score 17; DB 28; Length 56;
Best Local Similarity 76.9%; Pred. No. 3.2e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCGAAGT 27
Db 43 AATTTGTTTTTTAAACCGAATT 18

RESULT 5
BZ766643/c 45 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_137659.19.20.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_137659.19.20.x, genomic survey sequence.
ACCESSION BZ766643
VERSION BZ766643.1 GI:28939196
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 45)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)

TITLE JOURNAL
COMMENT

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES
source
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_137659.19.20.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 43.1%; Score 16.8; DB 28; Length 45;
Best Local Similarity 75.0%; Pred. No. 3.8e+04;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 7 TGAATTTTAAACCGAAGTCAAGAC 34
Db 44 TGAATATCATTAACCGAAGTCAAGATC 17

RESULT 6
BQ625561/c 51 bp mRNA linear EST 01-JUL-2002
LOCUS rd17c06.y1 Meloidogyne incognita egg S11 TOPO v1 Meloidogyne incognita cDNA 5', mRNA sequence.
DEFINITION BQ625561
ACCESSION BQ625561.1 GI:21652739
VERSION BQ625561
KEYWORDS EST.
SOURCE Meloidogyne incognita (southern root-knot nematode)
ORGANISM Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

REFERENCE 1 (bases 1 to 51)
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritzer, E., Bennett, J., Franklin, C., Tsagaris, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

TITLE JOURNAL
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Meloidogyne incognita eggs were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.
Putative full length read
The vector to vector length is 52
Seq primer: -40RP from Gibco.

FEATURES
source
1..51
/organism="Meloidogyne incognita"
/mol_type="mRNA"
/db_xref="taxon:6306"

/dev_stage="egg"
/lab_host="DH10B (Invitrogen)"
/clone_lib="Meloidegyme incognita egg SL1 TOPO v1"
/note="Vector: PCRIT-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCarty at Washington University,
St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR
products of size >400 nucleotides containing SL1 on the 5'
end and oligo(dT) on the 3' end were non-directionally
cloned into PCRIT-TOPO (Invitrogen) following the TOPO TA
cloning protocol. Meloidegyme incognita eggs were provided
by Andrew Kloeck of Divergence Inc., St. Louis, MO."

ORIGIN

Query Match 42.6%; Score 16.6; DB 13; Length 51;
Best Local Similarity 71.0%; Pred. No. 4.5e+04;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 6 CTGAATTTTAAACCCGAGTCAAGAGCTA 36
|||||
41 CTGATTTTGTAGACTTTTAACTCAAGAAATTA 11

RESULT 7

DME545095 54 bp DNA linear GSS 24-FEB-2003
LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
DEFINITION p{RS5}5-HA-1284, clone library P{RS5}, genomic survey sequence.
ACCESSION AJ545095
VERSION AJ545095.1 GI:28552782
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 Ryder, E.J., Ashburner, M., Bagunya, J., Blows, F., Bucheton, A.,
Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N.,
Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P.,
Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A.,
Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and
Russell, S.
Mapping of RS P element insertions in Drosophila melanogaster for
the Drosdel second generation deficiency kit
Unpublished
2 (bases 1 to 54)
Ryder, E.J.
Direct Submission
Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,
University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
The insertion point of the P element is before base 1 of the
sequence. Further information about this P element insertion line
can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>

AUTHORS

TITLE

Mapping of RS P element insertions in Drosophila melanogaster for
the Drosdel second generation deficiency kit
Unpublished

2 (bases 1 to 54)
Ryder, E.J.

JOURNAL

Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,
University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
The insertion point of the P element is before base 1 of the
sequence. Further information about this P element insertion line
can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>

COMMENT

Unpublished
2 (bases 1 to 54)
Ryder, E.J.
Direct Submission
Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,
University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM
The insertion point of the P element is before base 1 of the
sequence. Further information about this P element insertion line
can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>

FEATURES

source

1. 54
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="3L"
/clone="P{RS5}5-HA-1284"
/clone_lib="P{RS5}"
/note="read=5' end"
1. 54
/note="P element insertion in the 5' to 3' orientation"

ORIGIN

Query Match 42.6%; Score 16.6; DB 29; Length 54;
Best Local Similarity 71.0%; Pred. No. 4.5e+04;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 8 GAATTTTAAACCCGAGTCAAGAGCTAGT 38

Db

|||||
5 GAACATATGAACCCCTAATTACGATCTATT 35

RESULT 8

CL002273/c

LOCUS

CL002273 53 bp DNA linear GSS 19-DEC-2003
02S0105-04A1-A06 UniformMu MutTAIL Library Zea mays genomic clone

DEFINITION

02S0105-04A1-A06, genomic survey sequence.

ACCESSION

CL002273
CL002273.1 GI:40219352

VERSION

GSS.

KEYWORDS

Zea mays

SOURCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 53)
Latschaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
Sequence tagged transposon insertions from the UniformMu maize
population
Unpublished (2003)

JOURNAL

Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu

Sequence flanking probable Mu insertion site in UniformMu line:
02S0105-04, Primer set: A
Class: transposon insertion site.
Location/Qualifiers
1. 53
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="02S0105-04A1-A06"
/clone_lib="UniformMu MutTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

FEATURES

source

ORIGIN

Query Match 42.1%; Score 16.4; DB 29; Length 53;
Best Local Similarity 76.9%; Pred. No. 5.4e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTGAATTTTAAACCCGAGTCAAG 31
|||||

51 CCGAATTTCTGAACCTGATGTAAAG 26

RESULT 9

BZ665081/c

LOCUS

BZ665081 60 bp DNA linear GSS 31-JAN-2003
SALK_110684.14.10.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_110684.14.10.x, genomic
survey sequence.

ACCESSION

BZ665081
BZ665081.1 GI:28182384

VERSION

GSS.

KEYWORDS

Arabidopsis thaliana (thale cress)

SOURCE

Arabidopsis thaliana

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 60)

ORIGIN

QY	2	AACTCTGAATTTTAAACC	22
Db	37	ACCACTGAATTTTAAACTC	57

LOCUS	AU106257	50 bp	mRNA	linear	EST 30-AUG-2001
DEFINITION	AU106257	Sugano Homo sapiens	CDNA library	Homo sapiens	CDNA clone
ACCESSION	KAIA5073,	mRNA	sequence.		
	AU106257				

REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 149-156 (1997).

FEATURES	Location/Qualifiers
source	1. .50

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1.50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAIA5073"
/clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN

Query Match	41.0%;	Score 16;	DB 9;	Length 50;
Best Local Similarity	79.2%;	Pred. No. 7.7e+04;		
Matches 19;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

QY		6 CTGAATTTTAAAAACCGAAGTC A 29
Dd		27 CTGAAC TTTTA AA ACTCC CAGACA 50

RESULT 13	LOCUS	DEFINITION	LOCUS	DEFINITION
BQ786274	BQ786274	51 bp mRNA linear EST 26-JUL-2002	BQ786274	51 bp mRNA linear EST 26-JUL-2002
	saq65h01.y1 Gm-c1076 Glycine max CDNA clone SOYBEAN		saq65h01.y1 Gm-c1076 Glycine max CDNA clone SOYBEAN	
	Gm-c1076-4945 5', mRNA sequence.		Gm-c1076-4945 5', mRNA sequence.	

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BQ786274 BQ786274.1 EST. Glycine max Glycine max	GI:21994746 (soybean)
--	--	--

REFERENCE
AUTHORS
1 (bases 1 to 51)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvett, V.

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project

COMMENT	FEATURES
Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington Univerisity School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: cuu@resgen.com web site: www.resgen.com	Seq primer: -40RP from Gibco. Location/Qualifiers 1. .51

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/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl076-4945"
/tissue_type="wounded cotyledons"
/dev_stage="11 day old seedlings"
/lab_host="DH10B"
/clone_lib="Gm-cl076"

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/note="Vector: pBluescript II SK+; Site1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 11 day old seedlings treated with that were treated with 2 μ g/ml of a crude glucan elicitor preparation isolated from the mycelial walls of *Phytophthora sojae*. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into *E. coli* Electromax DH10B host cells. Plant material was provided by Michael G. Hahn (Complex Carbohydrate Research Center, University of Georgia) and the library was constructed by Anu Khanna (Tula Vodkin lab, University of Illinois)."

ORIGIN

Query Match	40.5%;	Score 15.8;	DB 13;	Length 51;
Best Local Similarity	89.5%;	Pred. No. 9.2e+04;		
Matches 17;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 TAACCTCTGAATTTTAAAA 19
 |||||
 Db 9 TAACCTCGTATTTTAAAA 27

RESULT 14	AA531325	52 bp	mrna	linear	EST 20-AUG-1997
LOCUS	AA531325				
DEFINITION	np151g04.s1 NCI CGAP Pr9 Homo sapiens cDNA clone IMAGE:196054 similar to SW:NU3M HUMAN P03897 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 ;, mrna sequence.				

ACCESSION	AA531325	GI:2274031
VERSION	AA531325.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
1 (bases 1 to 52)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuagui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.1nl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 528 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

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1. .52
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:996054"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr9"
/notes="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells, cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."

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ORIGIN

Query Match	40.5%	Score 15.8;	DB 9;	Length 52;
Best Local Similarity	65.7%;	Pred. No. 9.2e+04;		
Matches 23;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;

Dy 2 AACTCTGAATTTTAAACCCGGAAGTCAGAGCTA 36
 | | | | | | | | | | | | | | | |
Db 5 ATCACTACAATTGGACTACCACAACTCAACGGCTA 39

RESULT	15
W38842/c	
LOCUS	W38842
DEFINITION	59 bp mRNA linear EST 15-MAY-1996 zb28c08.r1 Soares parathyroid tumor MbHPA Homo sapiens cDNA clone

ACCESSION

VERSION W38842.1 GI:1320547
KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE AUTHORS

Euryarchonta; Metazoa; Choriata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 59)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Narra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL ; com

IMAGE Consortium (info@image.llnl.gov) for further information
Trace considered overall poor quality
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
Location/Qualifiers
1..59
FEATURES
source

FEATURES
Source

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/oranism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248320"
/db_xref="taxon:9606"
/clone="IMAGE:304910"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/notes="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCGACCAATTTTTTT
TTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

```

ORIGIN

Query Match	40.5%;	Score 15.8;	DB 14;	Length 59;
Best Local Similarity	65.7%;	Pred. No. 9.3e+04;		
Matches 23;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;

Dy 5 TCTGAATTTTAAACCCGAGTCAGAGCTAGTA 39
Dd 52 TCTGTCTTTAAATCACAATAAGAGCTGCTA 18

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Search completed: March 20, 2004, 12:20:59
Job time : 1994 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 11:43:07 ; Search time 1715 Seconds

(without alignments)
985.643 Million cell updates/sec

Title: US-09-435-471B-9
Perfect score: 39
Sequence: 1 taactctgaatttttaaacccgaagtcagagtagta 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1685580

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
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34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.6	47.7	47	6	AR288828 Sequence
C 2	17.2	44.1	51	6	AX165073 Sequence
C 3	17	43.6	20	6	AR076665 Sequence
C 4	17	43.6	20	6	I87134 Sequence 30
C 5	17	43.6	20	6	AR182722 Sequence
C 6	17	43.6	20	6	AR237069 Sequence
C 7	17	43.6	20	6	AR300802 Sequence
C 8	17	43.6	20	6	AX226320 Sequence
C 9	17	43.6	20	6	AX774418 Sequence
C 10	17	43.6	20	6	BD016021 Sequence
C 11	17	43.6	20	6	BD016140 Sequence
C 12	17	43.6	20	6	BD017292 Sequence
C 13	16.6	42.6	32	6	AR002639 Sequence
C 14	16.6	42.6	32	6	AR099689 Sequence
C 15	16	41.0	47	6	AX378298 Sequence
C 16	15.8	40.5	42	6	AX463216 Sequence
C 17	15.8	40.5	47	6	AR288585 Sequence
C 18	15.6	40.0	30	6	AX184137 Sequence
C 19	15.6	40.0	43	6	AX484624 Sequence
C 20	15.6	40.0	51	6	AX164997 Sequence
C 21	15.4	39.5	51	6	AX158820 Sequence
C 22	15.2	39.0	26	6	AX708066 Sequence
C 23	15.2	39.0	35	8	AJ587623 Sequence
C 24	15.2	39.0	38	6	AR052498 Sequence
C 25	15.2	39.0	39	6	I79583 Sequence 7
C 26	15.2	39.0	41	6	AX515592 Sequence
C 27	15.2	39.0	41	6	AX519852 Sequence
C 28	15.2	39.0	47	6	AR284723 Sequence
C 29	15.2	39.0	55	8	AJ528810 Arabidops
C 30	15	38.5	42	6	AR154181 Sequence
C 31	15	38.5	42	6	AR175508 Sequence
C 32	15	38.5	42	6	AR179283 Sequence
C 33	15	38.5	42	6	BD249391 Electroni
C 34	15	38.5	42	6	AR352390 Sequence
C 35	15	38.5	42	6	BD190466 AMPLIFICA
C 36	14.8	37.9	33	6	AR034456 Sequence
C 37	14.8	37.9	33	6	AR070401 Sequence
C 38	14.8	37.9	33	6	AR368986 Sequence
C 39	14.8	37.9	33	6	BD011018 HIV probe
C 40	14.8	37.9	39	6	AR014274 Sequence
C 41	14.8	37.9	39	6	AR103029 Sequence
C 42	14.8	37.9	39	6	E11500 Synthetic D
C 43	14.8	37.9	43	6	AX483506 Sequence
C 44	14.8	37.9	43	6	AX484539 Sequence
C 45	14.8	37.9	46	6	AR014278 Sequence

ALIGNMENTS

RESULT 1
AR288828/c
LOCUS AR288828 47 bp DNA
DEFINITION Sequence 563 from patent US 6537751.
ACCESSION AR288828
VERSION AR288828.1 GI:31676112
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 563 25-MAR-2003;


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FEATURES      Location/Qualifiers
              1. .47
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN
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Query Match	47.7%	Score 18.6;	DB 6;	Length 47;
Best Local Similarity	68.6%;	Pred. No. 4.8e+04;		
Matches 24;	Conservative 1;	Mismatches 10;	Indels 0;	Gaps 0;

```

2y      1 TAACCTCTGAATTTTAAACCCCGAAGTCAGAAGCT 35
          ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      46 TCACTAAAAATTTTTTTCACCTKAAGTCATAAGCT 122

```

RESULT 2	AXI65073	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	AXI65073	51 bp	DNA	linear	PAT 22-JUN-2001			
	Sequence	268	from Patent	WO0138586.				
	AXI65073							
	AXI65073.1	GI:14545902						
							Homo sapiens (human)	
							Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0138586-A 268 31-MAY-2001;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

FEATURES	Location/Qualifiers
source	1..51
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
variation	26
	/note="single nucleotide polymorphism"
	Accession number cg43999373"

Query Match	44.1%	Score 17.2;	DB 6;	Length 51;
Best Local Similarity	65.8%	Pred. No. 1.5e+05;		
Matches 25; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAAGTCAAGAGCTAGTA 39
| | | | | | | | | | | | | | | | | | | | | |
Db 6 AATTCAAGACTTTTCAACCCGAACTGGAGAAAGAGCA 43

RESULT 3			
AR076665/c			
LOCUS	AR076665	20 bp	DNA
DEFINITION	Sequence 30 from patent US 5959096.		linear
ACCESSION	AR076665		
VERSION	AR076665.1	GI:10003411	PAT 30-AUG-2000

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 20)
TITLE	Bennett, C. Frank. and Dean, N.
JOURNAL	Antisense oligonucleotides against human protein kinase C
FEATURES	Patent: US 5959096-A 30 28-SEP-1999;
source	Location/Qualifiers
	1. .20

Query Match	43.6%	Score 17;	DB 6;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 2.2e+05;		
ORIGIN	/organism="unknown" /mol_type="unassigned DNA"			

	Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	20	CCCCAAGTCAAGAGCTA	36							
Db	20	CCCCAAGTCAAGAGCTA	4							

RESULT 4			
I87134/c			
LOCUS	I87134	20 bp	DNA
DEFINITION	Sequence 30 from patent US 5703054.	linear	PAT 10-JUN-1998
ACCESSION	I87134		
VERSION	I87134.1	GI:3206852	

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 20)
TITLE	Bennett, C.Frank. and Dean, N.
JOURNAL	Oligonucleotide modulation of protein kinase C
FEATURES	Patent: US 5703054-A 30 30-DEC-1997;
source	Location/Qualifiers
	1. .20

Query Match	43.6%	Score 17;	DB 6;	Length 20;
Best Local Similarity	100.0%	Pred. No. 2.2e+05;		
Matches 17; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	20	CCCGAAGTCAAGAGCTA	36
Db	20	CCCGAAGTCAAGAGCTA	4

RESULT 5					
ARI182722/c	ARI182722	20 bp	DNA	linear	PAT 20-APR-2002
LOCUS	Sequence 30 from patent US 6339066.				
DEFINITION					
ACCESSION	ARI182722				
VERSION	ARI182722.1	GI:20225929			

REFERENCE	AUTHORS	TITLE
1	(bases 1 to 20)	Unclassified.
	Bennett, C. Frank., Dean, N.M., Cook, P. Dan. and Hoke, G.	Antisense oligonucleotides which have phosphorothioate linkages of high chiral purity and which modulate .beta.I, .beta.II, .gamma., .delta., .EPSILON., .zeta. and .eta. isoforms of human protein

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JOURNAL Patent: US 6339066-A 30 15-JAN-2002,
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

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Query Match	43.6%;	Score 17;	DB 6;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 2.2e+05;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	20	CCCGAAGTCAAGAGCTA	36	
Db	20	CCCGAAGTCAAGAGCTA	4	

RESULT 6	AR237069/c	AR237069	20 bp	DNA	linear	PAT 20-DEC-2002
LOCUS		Sequence	30	from patent US 6465439.		
DEFINITION		AR237069				
ACCESSION		AR237069				

VERSION AR237069.1 GI:27281727
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nicklin,P.L., Phillips,J.A., Love,W.G. and Hamilton,K.O.
TITLE Pharmaceutical compositions
JOURNAL Patent: US 6465439-A 30 15-OCT-2002;
FEATURES
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 7
LOCUS AR300802/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 30 from patent US 6537973.
ACCESSION AR300802
VERSION AR300802.1 GI:31688369
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F., Dean,N.M., Holmlund,J.T. and Dorr,F.A.
TITLE Oligonucleotide inhibition of protein kinase C
JOURNAL Patent: US 6537973-A 30 25-MAR-2003;
FEATURES
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 8
LOCUS AX226320/c 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 30 from Patent EP1126025.
ACCESSION AX226320
VERSION AX226320.1 GI:15555584
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bennett,C.F. and Dean,N.
TITLE Oligonucleotide modulation of protein kinase C
JOURNAL Patent: EP 1126025-A 30 22-AUG-2001;
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/note="Artificial"
ORIGIN

Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 9
LOCUS AX774418/c 20 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 30 from Patent EP1310555.
ACCESSION AX774418
VERSION AX774418.1 GI:32486070
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bennett,C.F. and Dean,N.
TITLE Oligonucleotide modulation of protein kinase C
JOURNAL Patent: EP 1310555-A 30 14-MAY-2003;
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 10
LOCUS BD016021/c 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-epsilon.
ACCESSION BD016021
VERSION BD016021.1 GI:22557159
KEYWORDS JP 2001224386-A/30.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-epsilon
JOURNAL Patent: JP 2001224386-A 30 21-AUG-2001;
COMMENT
OS Artificial Sequence
PN JP 2001224386-A/30
PD 21-AUG-2001
PF 13-DEC-2000 JP 2000379218
PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
C12N15/09,A61K48/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
G01N33/53,
PC G01N33/566,G01N33/573//A61K31/711,A61K31/712,A61K31/7125, PC
A61P35/00,
PC A61P43/00,A61P43/00,C12N5/10,C12N15/00,C12N5/00 CC synthetic
FH Key Location/Qualifiers
FT source 1. .20
FT Location/Qualifiers
/organism="Artificial Sequence".

Source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

RESULT 11
BD016140/c 20 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Oligonucleotide modulation of protein kinase C-zeta.
ACCESSION BD016140
VERSION BD016140.1 GI:22557278
KEYWORDS JP 2001224387-A/30.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, F.C., Boggs, R.T. and Dean, N.M.
TITLE Oligonucleotide modulation of protein kinase C-zeta
JOURNAL Patent: JP 2001224387-A 30 21-AUG-2001;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001224387-A/30
PD 21-AUG-2001
PE 13-DEC-2000 JP 2000379249
PR 09-JUL-1993 US 08/089996, 22-FEB-1994 US 08/199779 PI
FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
C12N15/09, A61K31/7088, A61K48/00, A61P29/00, A61P43/00, PC
C07H21/00,
PC C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N33/573//
PC C12N5/10, C12N15/00, C12N5/00
CC synthetic
FH Key
FT source
FT Location/Qualifiers
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1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

RESULT 12
BD017292/c 20 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Oligonucleotide modulation of protein kinase C-eta.
ACCESSION BD017292
VERSION BD017292.1 GI:22558468
KEYWORDS JP 2001231579-A/30.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, F.C., Boggs, R.T. and Dean, N.M.

TITLE
JOURNAL Oligonucleotide modulation of protein kinase C-eta
Patent: JP 2001231579-A 30 28-AUG-2001;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001231579-A/30
PD 28-AUG-2001
PE 13-DEC-2000 JP 2000379234
PR 09-JUL-1993 US 08/089996, 22-FEB-1994 US 08/199779 PI
FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
C12N15/09, A61K31/711, A61K31/712, A61K31/7125, A61K48/00, A61P29/00, A61P35/00,
PC A61P43/00, C07H21/00, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, PC
G01N33/50,
PC G01N33/53, G01N33/566//C12N5/10, G01N33/68, C12N15/00, C12N5/00 CC
synthetic
FH Key
FT source
FT Location/Qualifiers
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1..20
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 43.6%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

RESULT 13
AR002639/c 32 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 28 from patent US 5741899.
ACCESSION AR002639
VERSION AR002639.1 GI:3964193
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 32)
AUTHORS Capon, D.J., Tian, H., Smith, D.H., Winslow, G.A. and Siekevitz, M.
TITLE Chimeric receptors comprising janus kinase for regulating cellular
proliferation
JOURNAL Patent: US 5741899-A 28 21-APR-1998;
FEATURES
source Location/Qualifiers
1..32
/organism="Unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 42.6%; Score 16.6; DB 6; Length 32;
Best Local Similarity 71.0%; Pred. No. 2.8e+05;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 8 GAATTTTAAACCCGAGTCAAGAGCTAGT 38
DB 32 GAGCTTCTAAACTGGAAGTCGACAGTCAGT 2

RESULT 14
AR099689/c 32 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 28 from patent US 6077947.
ACCESSION AR099689
VERSION AR099689.1 GI:12809455
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Capon,D.J., Tian,H., Smith,D.H., Winslow,G.A. and Siekevitz,M.
 TITLE DNA encoding an intracellular chimeric receptor comprising Janus kinase

JOURNAL Patent: US 6077947-A 28 20-JUN-2000;
 FEATURES Location/Qualifiers
 source 1..32
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 42.6%; Score 16.6; DB 6; Length 32;
 Best Local Similarity 71.0%; Pred. No. 2.8e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 8 GAATTTTAAACCCGAGTCAAGAGCTAGT 38
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 Db 32 GAGCTTCTAAACTGGAAGTCGACAGTCAGT 2

RESULT 15

AX378298/c 47 bp DNA linear PAT 18-MAR-2002
 LOCUS AX378298
 DEFINITION Sequence 87 from Patent WO0206525.
 ACCESSION AX378298
 VERSION AX378298.1 GI:19574148
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.
 TITLE Obesity associated diallelic marker maps
 JOURNAL Patent: WO 0206525-A 87 24-JAN-2002;
 GENSET (FR)

FEATURES Location/Qualifiers
 source 1..47
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

variation

24 /note="99-26989-152 : polymorphic base C or T"

ORIGIN

Query Match 41.0%; Score 16; DB 6; Length 47;
 Best Local Similarity 64.7%; Pred. No. 4.3e+05;
 Matches 22; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 6 CTGAATTTTAAACCCGAGTCAAGAGCTAGTA 39
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 Db 47 CAGAATTTTAAATCAGGTGTCRCATTAAGTA 14

Search completed: March 20, 2004, 12:53:58
 Job time : 1719 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: March 20, 2004, 06:38:30 ; Search time 38 Seconds

(without alignments)
569.555 Million cell updates/sec

Title: US-09-435-471B-9
Perfect score: 39
Sequence: 1 taactctgaattttaaaccgaagtcagagtagta 39

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 874574

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued_Patents_NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	47.7	47	4	US-09-422-978-563 Sequence 563, Appl
2	17	43.6	20	1	US-08-089-996-30 Sequence 30, Appl
3	17	43.6	20	2	US-08-478-178A-30 Sequence 30, Appl
4	17	43.6	20	2	US-08-488-177-30 Sequence 30, Appl
5	17	43.6	20	2	US-08-481-072A-30 Sequence 30, Appl
6	17	43.6	20	2	US-08-664-336-30 Sequence 30, Appl
7	17	43.6	20	2	US-08-481-066A-30 Sequence 30, Appl
8	17	43.6	20	3	US-08-578-615A-30 Sequence 30, Appl
9	17	43.6	20	4	US-08-829-637A-30 Sequence 30, Appl
10	17	43.6	20	4	US-09-254-322-30 Sequence 30, Appl
11	17	43.6	20	4	US-10-025-139-30 Sequence 30, Appl
12	17	43.6	20	5	PCT-US93-02213-30 Sequence 30, Appl
13	17	43.6	20	5	PCT-US94-07770-30 Sequence 30, Appl
14	16.6	42.6	32	1	US-08-481-003-28 Sequence 28, Appl
15	16.6	42.6	32	3	US-08-485-598-28 Sequence 28, Appl
16	15.8	40.5	47	4	US-09-422-978-320 Sequence 320, Appl
17	15.8	40.5	60	4	US-09-894-844-132 Sequence 132, Appl
18	15.8	40.5	60	4	US-09-894-844-133 Sequence 133, Appl
19	15.2	39.0	38	2	US-08-709-923-5 Sequence 5, Appl
20	15.2	39.0	39	1	US-08-433-037-7 Sequence 7, Appl
21	15.2	39.0	47	4	US-09-671-317-775 Sequence 775, Appl
22	15	38.5	42	3	US-09-290-577-21 Sequence 21, Appl
23	15	38.5	42	4	US-09-290-452-21 Sequence 21, Appl
24	15	38.5	42	4	US-09-290-338-21 Sequence 21, Appl
25	15	38.5	42	4	US-09-290-000-21 Sequence 21, Appl
26	15	38.5	42	4	US-09-954-594A-21 Sequence 21, Appl
27	14.8	37.9	33	2	US-08-479-275D-38 Sequence 38, Appl

28	14.8	37.9	33	2	US-08-488-271B-38	Sequence 38, Appl	
C	29	14.8	37.9	33	4	US-08-169-715-38	Sequence 38, Appl
C	30	14.8	37.9	39	1	US-08-537-002A-6	Sequence 6, Appl
C	31	14.8	37.9	39	3	US-08-863-010-6	Sequence 6, Appl
C	32	14.8	37.9	39	3	US-09-024-429-6	Sequence 6, Appl
C	33	14.8	37.9	46	1	US-08-537-002A-10	Sequence 10, Appl
C	34	14.8	37.9	46	3	US-08-863-010-10	Sequence 10, Appl
C	35	14.8	37.9	46	3	US-09-024-429-10	Sequence 10, Appl
C	36	14.8	37.9	47	4	US-09-671-317-683	Sequence 683, Appl
C	37	14.8	37.9	50	1	US-08-171-389-517	Sequence 517, Appl
C	38	14.8	37.9	50	1	US-08-123-936-517	Sequence 517, Appl
C	39	14.8	37.9	50	2	US-08-475-228A-517	Sequence 517, Appl
C	40	14.8	37.9	50	3	US-08-482-080A-517	Sequence 517, Appl
C	41	14.8	37.9	50	4	US-09-354-947-517	Sequence 517, Appl
C	42	14.8	37.9	50	5	PCT-US93-12388-517	Sequence 517, Appl
C	43	14.6	37.4	33	1	US-08-148-058A-23	Sequence 23, Appl
C	44	14.6	37.4	33	1	US-08-148-058A-24	Sequence 24, Appl
C	45	14.6	37.4	33	1	US-08-478-042-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-422-978-563/C
; Sequence 563, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density....
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422, 978
; EARLIER FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298, 850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109, 732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082, 614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 563
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-15441-337 : polymorphic base A or C
US-09-422-978-563

Query Match 47.7%; Score 18.6; DB 4; Length 47;
Best Local Similarity 68.6%; Pred. No. 66;
Matches 24; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

CY 1 TAACTCTGAATTTTAAACCCGAAGTCAAGAGCT 35
Db 46 TCACTAAATTTTTCACCTKAAAGTCATAAGCT 12

RESULT 2
US-08-089-996-30/C
; Sequence 30, Application US/08089996
; Patent No. 5703054
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5703054ris

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,996
FILING DATE: 19930709
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumont
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-089-996-30

Query Match 43.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 3
US-08-478-178A-30/c
Sequence 30, Application US/08478178A
Patent No. 5882927
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5882927ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,178A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumont

REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-478-178A-30

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 4
US-08-488-177-30/c
Sequence 30, Application US/08488177
Patent No. 5885970
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5885970ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-488-177-30

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36

Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 5

US-08-481-072A-30/c

; Sequence 30, Application US/08481072A
; Patent No. 5916807

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonucleotide Modulation of

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

ADDRESS: Mackiewicz & No. 5916807ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,072A

FILING DATE: herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaumont

REGISTRATION NUMBER: 35,152

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ANTI-SENSE: yes

US-08-481-072A-30

Query Match 43.6%; Score 17; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36

Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 6

US-08-664-336-30/c

; Sequence 30, Application US/08664336
; Patent No. 5922686

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonucleotide Modulation of Protein

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

ADDRESS: Mackiewicz & No. 5922686ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/664,336

FILING DATE: herewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 089,996

FILING DATE: July 9, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: ISIS-2345

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ANTI-SENSE: yes

US-08-664-336-30

Query Match 43.6%; Score 17; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36

Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 7

US-08-481-066A-30/c

; Sequence 30, Application US/08481066A
; Patent No. 5959096

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett

TITLE OF INVENTION: Oligonucleotide Modulation of

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

ADDRESS: Mackiewicz & No. 5959096ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,066A

FILING DATE: herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaumont

REGISTRATION NUMBER: 35,152

```

REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-481-066A-30

```

```

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

```

```

RESULT 8
US-08-578-615A-30/c
Sequence 30, Application US/08578615A
Patent No. 6015892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz MacKiewicz & No. 6015892r1s LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-578-615A-30

```

```

Query Match 43.6%; Score 17; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 20 CCCGAGTCAAGAGCTA 36
DB 20 CCCGAGTCAAGAGCTA 4

```

```

RESULT 9
US-08-829-637A-30/c
Sequence 30, Application US/08829637A
Patent No. 6339066
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Phillip Dan Cook
APPLICANT: Nicholas Dean
APPLICANT: Glenn Hoke
TITLE OF INVENTION: OLIGONUCLEOTIDES WHICH HAVE
TITLE OF INVENTION: PHOSPHOROTHIOMATE LINKAGES OF HIGH CHIRAL PURITY AND
TITLE OF INVENTION: WHICH MODULATE at, all, 'k, n, AND ISOFORMS OF
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Caldwell (28,937) Woodcock
STREET: Washburn Kurtz MacKiewicz & No. 6339066r1s
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,637A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,066
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,129
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,851
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,569
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/089,996
FILING DATE: 09-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/058,023
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,007
FILING DATE: 16-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,760
FILING DATE: 15-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,852
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00243
FILING DATE: 11-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,977
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,358
FILING DATE: 11-JAN-1990
ATTORNEY/AGENT INFORMATION:

```


NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: ISIS-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
US-08-829-637A-30

Query Match 43.6%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
Db 20 CCCGAGTCAAGAGCTA 4

RESULT 10
US-09-254-322-30/c
Sequence 30, Application US/09254322
Patent No. 6465439
GENERAL INFORMATION:
APPLICANT: Nicklin, Paul
APPLICANT: Phillips, Judith
APPLICANT: Love, William
APPLICANT: Hamilton, Karen
TITLE OF INVENTION: Pharmaceutical Compositions
FILE REFERENCE: 4-21026/MA 2138/PCT
CURRENT APPLICATION NUMBER: US/09/254,322
CURRENT FILING DATE: 1999-03-04
EARLIER APPLICATION NUMBER: PCT/EP97/04796
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 30
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-254-322-30

Query Match 43.6%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
Db 20 CCCGAGTCAAGAGCTA 4

RESULT 11
US-10-025-139-30/c
Sequence 30, Application US/10025139
Patent No. 6537973
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Holmlund, Jon T.
APPLICANT: Dorr, F. Andrew
TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
FILE REFERENCE: ISIS4954
CURRENT APPLICATION NUMBER: US/10/025,139
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 08/829,637

PRIOR FILING DATE: 1997-03-31
PRIOR APPLICATION NUMBER: US 08/478,178
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/089,996
PRIOR FILING DATE: 1993-07-09
PRIOR APPLICATION NUMBER: US 07/852,852
PRIOR FILING DATE: 1992-03-16
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentln version 3.1
SEQ ID NO 30
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-025-139-30

Query Match 43.6%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
Db 20 CCCGAGTCAAGAGCTA 4

RESULT 12
PCT-US93-02213-30/c
Sequence 30, Application PC/TUS9302213
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of Protein
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02213
FILING DATE: 19930225
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISIS-0872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
PCT-US93-02213-30

Query Match 43.6%; Score 17; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
 Db 20 CCCGAGTCAAGAGCTA 4

RESULT 13

PCT-US94-07770-30/c
 ; Sequence 30, Application PC/TUS9407770

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett and
 APPLICANT: Russell T. Boggs

TITLE OF INVENTION: Oligonucleotide Modulation of
 KINASE C

TITLE OF INVENTION: Protein

NUMBER OF SEQUENCES: 119

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Woodcock Washburn Kurtz

ADDRESSEE: Mackiewicz & Norris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

MEDIUM TYPE: STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07770

FILING DATE: herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

APPLICATION NUMBER: 08/089,996

FILING DATE: July 9, 1993

APPLICATION NUMBER: 08/199,779

FILING DATE: February 22, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaudond

REGISTRATION NUMBER: 35,152

REFERENCE/DOCKET NUMBER: ISIS-1546

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ANTI-SENSE: Yes

PCT-US94-07770-30

Query Match

Best Local Similarity 43.6%; Score 17; DB 5; Length 20;

Matches 17; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36

Db 20 CCCGAGTCAAGAGCTA 4

RESULT 14

US-08-481-003-28/c

; Sequence 28, Application US/08481003

; Patent No. 5741899

; GENERAL INFORMATION:

APPLICANT: CAPON, DANIEL J

APPLICANT: TIAN, HUAN

APPLICANT: SMITH, DOUGLAS H

APPLICANT: WINSLOW, GENINE A
 APPLICANT: SIEKEVITZ, MIRIAM
 TITLE OF INVENTION: CHIMERIC RECEPTORS FOR REGULATING
 CELLULAR PROLIFERATION AND EFFECTOR FUNCTION

TITLE OF INVENTION: CELLULAR PROLIFERATION AND EFFECTOR FUNCTION

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESSES:

ADDRESSEE: CELL GENESYS, INC.

STREET: 322 LAKESIDE DRIVE

CITY: FOSTER CITY

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,003

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/382,846

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: KRUPEN, KAREN I

REGISTRATION NUMBER: 34,647

REFERENCE/DOCKET NUMBER: CELL 17

TELEPHONE: (415) 358-9600 x131

TELEFAX: (415) 349-7392

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-481-003-28

Query Match

Best Local Similarity 42.6%; Score 16.6; DB 1; Length 32;

Matches 22; Conservativity 0; Mismatches 9; Indels 0; Gaps 0;

QY 8 GAATTTTAAACCCGAGTCAAGAGCTAGT 38

Db 32 GAGCTTCTAAACTGGAAGTCGACAGTCACT 2

RESULT 15

US-08-485-598-28/c

; Sequence 28, Application US/08485598

; Patent No. 6077947

; GENERAL INFORMATION:

APPLICANT: CAPON, DANIEL J

APPLICANT: TIAN, HUAN

APPLICANT: SMITH, DOUGLAS H

APPLICANT: WINSLOW, GENINE A

APPLICANT: SIEKEVITZ, MIRIAM

TITLE OF INVENTION: CHIMERIC RECEPTORS FOR REGULATING

CELLULAR PROLIFERATION AND EFFECTOR FUNCTION

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESSES:

ADDRESSEE: CELL GENESYS, INC.

STREET: 322 LAKESIDE DRIVE

CITY: FOSTER CITY

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

```

1 SOFTWARE: PatentIn Release #1.0, Version #1.23
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: US/08/485,598
4 FILING DATE:
5 CLASSIFICATION: 536
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US/08/382,846
8 FILING DATE:
9 ATTORNEY/AGENT INFORMATION:
10 NAME: KRUPEN, KAREN I
11 REGISTRATION NUMBER: 34,647
12 REFERENCE/DOCKET NUMBER: CELL 17
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (415) 358-9600 x131
15 TELEFAX: (415) 349-7392
16 INFORMATION FOR SEQ ID NO: 28:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 32 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: single
21 TOPOLOGY: linear
22 MOLECULE TYPE: DNA (genomic)
23 US-08-485-598-28

```

Query Match	42.6%;	Score 16.6;	DB 3;	Length 32;
Best Local Similarity	71.0%;	Pred. No. 4.1e+02;		
Matches 22;	Conservative 0;	Mismatches 9;	Indels 0;	Gaps 0;

Dy 8 GAATTTTAAACCCGAAGTCAGAGCTAGT 38
Db 32 GAGCTTCTAATACTGGAAGTCGACAGTCACT 2

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Search completed: March 20, 2004, 08:43:33
Job time : 40 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:43:35 ; Search time 243 Seconds

(without alignments)
681.810 Million cell updates/sec

Title: US-09-435-471B-9

Perfect score: 39

Sequence: 1 taactctgaatttttaaacccgaagtcagagtagta 39

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3308108

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19.4	49.7	50	6	ABZ05319	Abz05319 Human leu
2	17.4	44.6	47	3	AAZ66216	Aaz66216 Human map
3	17.2	44.1	51	5	ABL00277	Abi00277 Human sil
4	17	43.6	20	2	AAQ49686	Aaq49686 PKC-beta
5	17	43.6	20	2	AAQ97903	Aaq97903 PNA oligo
6	17	43.6	20	2	AAQ84190	Aaq84190 PKC-beta
7	17	43.6	20	2	AAV35530	Aav35530 Oligo ON3
8	17	43.6	20	2	AAZ22591	Aaz22591 Human pro
9	17	43.6	20	2	AAZ78553	Aaz78553 Human PKC
10	17	43.6	20	2	AAZ83662	Aaz83662 Human pro
11	17	43.6	20	2	AAZ19156	Aaz19156 Human PKC
12	17	43.6	20	2	AAZ27295	Aaz27295 Human pro
13	17	43.6	20	6	ABL90883	Abi90883 Human pro
14	17	43.6	20	4	ACH11162	Ach11162 Human pro
15	17	43.6	26	4	AAF70175	Aaf70175 Human TNF
16	16.8	43.1	50	6	ABZ05659	Abz05659 Human leu
17	16.6	42.6	32	2	AAT33501	Aat33501 PCR prime
18	16.6	42.6	51	4	AAL27388	Aal27388 Human SNP
19	16	41.0	25	8	ACI01214	Act01214 Human mic
20	16	41.0	47	6	ABK40839	Abk40839 Human cde
21	15.8	40.5	42	6	ABQ82194	Abq82194 Human CD8
22	15.8	40.5	45	4	AAC82264	Aac82264 Human ret
23	15.8	40.5	50	6	ABZ02741	Abz02741 Human leu

24	15.8	40.5	50	6	ABZ01361	Abz01361 Human leu
25	15.8	40.5	50	6	ABZ04957	Abz04957 Human leu
26	15.8	40.5	60	6	ABN40377	Abn40377 Human spl
27	15.6	40.0	25	8	ACT19196	Act19196 Human mic
28	15.6	40.0	30	4	AAH91564	Aah91564 Human inf
29	15.6	40.0	41	6	ABZ49267	Abz49267 Human ald
30	15.6	40.0	41	6	ABZ45006	Abz45006 Human ald
31	15.6	40.0	43	6	ABZ27977	Abz27977 Candida e
32	15.6	40.0	50	7	ACC83177	Acc83177 PCR prime
33	15.6	40.0	51	5	ABL00201	Abi00201 Human sil
34	15.4	39.5	31	2	AAV67919	Aav67919 Nucleotid
35	15.4	39.5	51	4	AAT75207	Aat75207 Human sil
36	15.4	39.5	60	6	ABN39178	Abn39178 Human spl
37	15.2	39.0	26	7	ACC90636	Acc90636 Human cyp
38	15.2	39.0	38	2	AAT84539	Aat84539 BIRK 10 P
39	15.2	39.0	41	6	ABL42413	Abi42413 L1 factor
40	15.2	39.0	51	4	AAL32249	Aal32249 Human SNP
41	15.2	39.0	56	2	AAZ11567	Aaz11567 Human bia
42	15	38.5	42	3	AAC64821	Aac64821 Novel str
43	15	38.5	42	3	AAC63142	Aac63142 Novel str
44	15	38.5	42	3	AAC65232	Aac65232 Allele-sp
45	15	38.5	42	3	AAC65165	Aac65165 Novel str

ALIGNMENTS

RESULT 1	
ID	ABZ05319 standard, DNA; 50 BP.
XX	ABZ05319;
AC	09-JAN-2003 (first entry)
DT	Human leukocyte gene expression profiling probe SEQ ID NO 5310.
DE	T7; leukocyte; gene expression profiling; allograft rejection;
XX	atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW	rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW	ss.
XX	Homo sapiens.
OS	WO200257414-A2.
PN	25-JUL-2002.
XX	22-OCT-2001; 2001WO-US047856.
PF	20-OCT-2000; 2000US-0241994P.
XX	08-JUN-2001; 2001US-0296764P.
PR	(BIOC-) BIOCARDIA INC.
XX	Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI	Ly N, Woodward R, Quentermou T, Johnson F;
XX	WPI; 2002-636525/68.
DR	New system for leukocyte expression profiling, diagnosing a disease, or
XX	monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT	or congestive heart failure, comprises diagnostic oligonucleotides.
PT	Claim 1; Page 499; Opp; English.
PS	The invention relates to a system for detecting gene expression, which
CC	comprises one or two isolated DNA molecules that detect expression of a
CC	gene, where the gene corresponds to any of 8143 oligonucleotides
CC	(ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC	for leukocyte expression profiling. It is particularly useful for
CC	diagnosing a disease, monitoring (rate of) progression of a disease,
CC	predicting therapeutic outcome, determining prognosis for a patient,

CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 15 A; 11 C; 7 G; 17 T; 0 U; 0 Other;

Query Match 49.7%; Score 19.4; DB 6; Length 50;
Best Local Similarity 79.3%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 AACTCTGAATTTTAAACCCGAAGTCAA 30
DB 4 AAGTTGAATTTGTCAAATCCCAAGTCAA 32

RESULT 2
AAZ66216/c
ID AAZ66216 standard; DNA; 47 BP.
XX
AC AAZ66216;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:563.
XX
KM Human genome; diallelic marker; high density disequilibrium map;
KM genomic map; haplotype; phenotype; polymorphic base; genotyping;
KM haplotyping; hybridisation; identification; characterisation; diagnosis;
KM single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel diallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 1; Page 350; 2745pp; English.
XX
CC AAZ66564 to AAZ69578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention
XX
SQ Sequence 47 BP; 19 A; 2 C; 12 G; 14 T; 0 U; 0 Other;

Query Match 44.6%; Score 17.4; DB 3; Length 47;
Best Local Similarity 68.6%; Pred. No. 2.3e+03;
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 TAACTCTGAATTTTAAACCCGAAGTCAAGACT 35
DB 46 TCACTAAAAAATTTTTCACCTTAAGTCATTAAGCT 12

RESULT 3
ABL00277
ID ABL00277 standard; DNA; 51 BP.
XX
AC ABL00277;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:268.
XX
KM Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KM autoimmune disease; inflammation; cancer; nervous system disease;
KM infection; polymorphic protein; ds.
XX
OS Homo sapiens.
XX
PN WO200138586-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032311.
XX
PR 24-NOV-1999; 99US-0167383P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-355949/37.
XX
PT Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
PS Claim 1; Page 328; 674pp; English.
XX
CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
SQ Sequence 51 BP; 16 A; 15 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 44.1%; Score 17.2; DB 5; Length 51;
Best Local Similarity 65.8%; Pred. No. 2.8e+03;
Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAAAGTCAAGAGCTAGTA 39
DB 6 AATTCAGAACTTTTTCACCCGAACTGGAGAGAGCA 43

RESULT 4

AAQ49686/c
ID AAQ49686 standard; DNA; 20 BP.

XX AAQ49686;

DT 25-MAR-2003 (revised)
DT 25-APR-1994 (first entry)

DE PKC-beta type II 3'-UTR binding oligomer 2160-2141.

XX Antisense; oligonucleotide; inter-sugar linkage; protein kinase C;
KW phosphorothionate linkage; PKC; transcription initiation site;
KW translation initiation site; 5' cap region; intron/exon boundary;
KW diagnosis; therapeutics; prophylaxis; ss.

XX Synthetic.

XX Key Location/Qualifiers
FT misc_feature 1..20 a
FT /note= "Phosphorothionate linkages"

PN WO9319203-A1.

PD 30-SEP-1993.

PF 25-FEB-1993; 93WO-US002213.

PR 16-MAR-1992; 92US-00852852.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Dean N;

DR WPI; 1993-320768/40.

PT Oligo-nucleotide(s) able to be hybridised with nucleic acids encoding PKC
PT - useful as diagnostics and therapeutics for disease states associated
PT with particular isoforms of protein Kinase C.

PS Claim 6; Page 19; 64pp; English.

XX The sequences given in AAQ49657-707 are antisense oligonucleotides which
CC contain altered inter-sugar linkages, pref. phosphorothionate linkages.
CC These oligomers bind with the protein kinase C (PKC) mRNA at the
CC transcription initiation site, the translation initiation site, the 5'
CC cap region, an intron/exon boundary, coding sequences or sequences in the
CC 5' or 3'-untranslated regions. These oligonucleotides may be used in
CC diagnostics, therapeutics, prophylaxis and as research reagents. The
CC numbers allocated to the oligonucleotides are relative to the first
CC residue to be sequenced on the cDNA, which is 28 residues upstream of the
CC ATG start codon. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

QY Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 20 CCCGAAAGTCAAGAGCTA 36
20 CCCGAAAGTCAAGAGCTA 4

RESULT 5
AAQ97903/c

ID AAQ97903 standard; DNA; 20 BP.

XX AAQ97903;

DT 25-MAR-2003 (revised)
DT 17-OCT-1995 (first entry)

DE PNA oligomer targeting 3' UTR region of PKC-beta isoform II.

XX Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss;
KW cell proliferation; cell differentiation; isozyme; antisense;
KW triple helix; cancer; psoriasis; inflammation.

XX Synthetic.

XX Key Location/Qualifiers
FT misc_feature 1..20 a
FT /note= "at least one (and preferably all) of the backbone
FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine
FT peptide residues, the nucleobase being attached
FT covalently to the acetyl group and the peptide linkage
FT being formed by condensation of the glycine carboxy group
FT of one residue with the amino group of the 2-aminoethyl
FT moiety in the next residue"

PN WO9503833-A1.

PD 09-FEB-1995.

PF 28-JUL-1994; 94WO-US008465.

PR 29-JUL-1993; 93US-00099098.

PA (ISIS-) ISIS PHARM INC.

PI Dean NM;

DR WPI; 1995-082040/11.

PT New peptide nucleic acid oligomers specific for protein kinase C
PT isozyme(s) - useful as anti:sense molecules for treating PKC mediated
PT disease, e.g. cancer, psoriasis and inflammation.

PS Claim 10; Page 261; 287pp; English.

XX New peptide nucleic acid (PNA) oligomers are provided which (a) consist
CC of naturally occurring nucleobases covalently bound to a polyamide
CC backbone and (b) hybridise to the translation initiation AUG region,
CC coding region, 5' untranslated region (5' UTR) or 3' untranslated region
CC (3' UTR) of PKC-alpha or its isoforms. The PNAs can be used to target RNA
CC and single stranded DNA (ssDNA) to produce antisense-type gene regulation
CC moieties. They inhibit expression of PKC-alpha and its isoforms
CC (including beta, gamma, delta, epsilon, zeta and eta) and so are useful
CC for treating and diagnosing cell proliferation and differentiation
CC processes such as neoplastic, hyperproliferative and inflammatory
CC diseases. PNA oligomers have high affinity for complementary single
CC stranded DNA. They are also able to form triple helices in which a first
CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the
CC resulting double helix or with the first PNA strand. The PNAs possess no
CC significant charge and are water soluble, which facilitates cellular
CC uptake. Further, since they contain amides of non-biological amino acids,
CC they are biostable and resistant to enzymatic degradation by proteases.
CC The present sequence targets the 3' UTR region of PKC-beta isoform II.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

QY Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 20 CCCGAAAGTCAAGAGCTA 36
20 CCCGAAAGTCAAGAGCTA 36

ID 20 CCGGAGTCAAGAGCTA 4

RESULT 6

AAQ84190/c
ID AAQ84190 standard; DNA; 20 BP.

AC AAQ84190;

DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)

DE PKC-beta type II antisense oligo, binds to cDNA bases 2141-2160.

KW Antisense; protein kinase C; alpha; PKC; beta; gamma; eta; epsilon; zeta;
KW modulation; expression; isozyme; hybridise; 5' UTR; human;
KW 3' untranslated region; translation initiation site; detection;
KW phosphorothioate linkage; 2'-O-methyl modification;
KW 2'-O-propyl modification; ss.

OS Synthetic.

PN WO9502069-A1.

PD 19-JAN-1995.

PF 08-JUL-1994; 94WO-US0077770.

PR 09-JUL-1993; 93US-00089996.

PR 22-FEB-1994; 94US-00199779.

XX (ISIS-) ISIS PHARM INC.

PI Bennett CF, Boggs RT, Dean NM;

DR WPI; 1995-066911/09.

PT Oligo:nucleotide(s) hybridisable with Protein Kinase C mRNA or gene -
PT also novel PKC-alpha 3'-UTR sequence, useful for diagnosis and treatment
PT of hyperproliferative disorders.
PS Claim 13; Page 27; 125pp; English.

CC The sequences given in AAQ84190-94 are oligos which are antisense to the
CC protein kinase C-beta (PKC-beta) type II cDNA. These oligos are antisense
CC to regions in the 3' untranslated region of the cDNA. The type I and type
CC II PKC-beta cDNA's are identical at the 5' end but diverge at the 3' end.
CC These antisense molecules may be used in modulating the expression of
CC this particular isozyme of PKC. These oligos preferably hybridise with
CC the 5'- or 3'-untranslated regions of the PKC gene, or the translation
CC initiation site, or the coding region. These oligos may be used in the
CC detection of the human PKC genes and for treatment of animals which have
CC conditions associated with PKC, esp. hyperproliferative diseases such as
CC psoriasis, colorectal cancer, lung cancer, breast or skin cancer. These
CC oligos may contain at least one phosphorothioate linkage and/or at least
CC one of the nucleotides comprises a modification on the 2' position of the
CC sugar, esp. a 2'-O-methyl or a 2'-O-propyl modification. (Updated on 25-
CC MAR-2003 to correct PN field.)

XX SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 CCGGAGTCAAGAGCTA 36
Db 20 CCGGAGTCAAGAGCTA 4

RESULT 7
AAV35530/c

ID AAV35530 standard; DNA; 20 BP.

AC AAV35530;

DT 01-SEP-1998 (first entry)

DE Oligo ON30 targeted to human protein kinase C (PKC)-beta type II.

KW Protein kinase C; PKC; target; hybridisation; human; liposome;
KW sterically stabilised; neoplastic disorder; inflammatory disorder;
KW hyperproliferative disorder; cancer; psoriasis; PKC-beta; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9809633-A2.

PD 12-MAR-1998.

PF 03-SEP-1997; 97WO-EP004796.

PR 04-SEP-1996; 96GB-00018376.

XX (NOVS) NOVARTIS AG.

PI Nicklin PL, Phillips JA, Love WC, Hamilton KO;

DR WPI; 1998-260955/23.

PT Oligo:nucleotide compositions for protein kinase C disorders - comprising
PT sequence hybridisable to protein kinase C gene entrapped in sterically
PT stabilised liposomes.
PS Claim 21; Page 8; 25pp; English.

CC This represents an oligonucleotide sequence that is specifically
CC hybridisable with DNA or RNA derived from a protein kinase C (PKC) gene,
CC entrapped in sterically stabilised liposomes. Compositions comprising
CC such oligonucleotides can be used in the treatment of PKC disorders and
CC for modulating the expression of PKC in cells. They can be used in the
CC diagnosis and treatment of disorders associated with PKC, particularly
CC neoplastic, inflammatory and hyperproliferative disorders such as cancer
CC or psoriasis. The compositions retain high activity after prolonged
CC circulation in the bloodstream and exhibit reduced accumulation of
CC oligonucleotides in non-target organs such as the liver and kidney

XX SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 CCGGAGTCAAGAGCTA 36
Db 20 CCGGAGTCAAGAGCTA 4

RESULT 8

AAV35530/c
ID AAV35530 standard; DNA; 20 BP.

AC AAV35530;

DT 27-MAY-1999 (first entry)

DE Human protein kinase C antisense oligonucleotide #30.

KW Protein kinase C; PKC; human; antisense; primer; inhibitor; treatment;
KW hyperproliferative condition; cancer; colorectal; breast; bladder; lung;
KW brain; glioblastoma multiforme; skin; psoriasis; ss.

OS Synthetic.
OS Homo sapiens.

XX PN US5885970-A.
XX PD 23-MAR-1999.
XX PF 07-JUN-1995; 95US-00488177.
XX PR 16-MAR-1992; 92US-00852852.
XX PR 09-JUL-1993; 93US-00089996.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dean N, Bennett CF;
XX DR WPI; 1999-228583/19.
XX PT New human protein kinase C antisense oligonucleotides - useful for
PT treating PKC-related hyperproliferative conditions e.g. cancer and
PT psoriasis.
XX PS Example 4; Col 15; 55pp; English.
XX CC This invention describes antisense oligonucleotides that specifically
CC bind to human protein kinase C (PKC) mRNA. These oligonucleotides can be
CC used to inhibit PKC mRNA and therefore be used to treat PKC-related
CC hyperproliferative conditions, e.g. cancer, especially colorectal cancer,
CC breast cancer, bladder cancer, lung cancer, or brain cancer (preferably
CC glioblastoma multiforme). The products of the invention may also be used
CC to treat skin cancer and psoriasis
XX SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
QY Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4
RESULT 9
AAx78553/c
ID AAX78553 standard; DNA; 20 BP.
XX AC AAX78553;
XX DT 03-SEP-1999 (first entry)
XX DE Human PKC-beta type II oligonucleotide primer #1.
XX KW PKC; human; PKC-alpha; primer; protein kinase C; expression modulator;
KW PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-eta; PKC-delta;
KW PKC-epsilon; PKC-zeta; anti-inflammatory; cytostatic;
KW antisense targeting; isozyme; growth control; hyperproliferative disease;
KW colon cancer; glioblastoma; bladder cancer; inflammatory condition;
KW psoriasis; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5922686-A.
XX PD 13-JUL-1999.
XX PF 14-JUN-1996; 96US-00664336.
XX PR 16-MAR-1992; 92US-00852852.
XX PR 09-JUL-1993; 93US-00089996.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dean N, Bennett CF;

XX DR WPI; 1999-404471/34.
XX PT Oligonucleotides targetted against nucleic acids encoding protein kinase
PT C.
XX PS Example 4; Col 41-42; 56pp; English.
XX CC This invention describes novel oligonucleotides (AAX78524-X78644) having
CC up to 50 nucleotides hybridisable with, and able to modulate the
CC expression of, a nucleic acid encoding protein kinase C and its isozymes
CC alpha, beta type I, beta type II, gamma, eta, delta, epsilon and zeta.
CC The oligonucleotides of the invention have anti-inflammatory and
CC cytostatic activity and are used for antisense targeting to modulate the
CC expression of PKC or of a particular PKC isozyme or set of isozymes in
CC cells or tissues. The products of the invention also hybridise with
CC nucleic acids involved in the modulation of PKC expression, which is
CC known to be involved growth control in hyperproliferative diseases e.g.
CC colon cancer, glioblastoma and bladder cancer as well as in inflammatory
CC conditions e.g. psoriasis. Due to their specificity the oligonucleotides
CC are able to overcome the problems of toxicity associated with previous
CC agents designed to modulate PKC expression
XX SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
QY Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 20 CCCGAAGTCAAGAGCTA 36
20 CCCGAAGTCAAGAGCTA 4
RESULT 10
AAX83662/c
ID AAX83662 standard; DNA; 20 BP.
XX AC AAX83662;
XX DT 27-AUG-1999 (first entry)
XX DE Human protein kinase C antisense oligonucleotide SEQ ID NO:30.
XX KW Human; protein kinase C; PKC; antisense oligonucleotide; diagnosis; ss;
KW hybridisation; cancer; psoriasis; hyperproliferative disease; tumour.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5916807-A.
XX PD 29-JUN-1999.
XX PF 07-JUN-1995; 95US-00481072.
XX PR 16-MAR-1992; 92US-00852852.
XX PR 09-JUL-1993; 93US-00089996.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dean N, Bennett CF;
XX DR WPI; 1999-403817/34.
XX PT New antisense oligonucleotides specific for human protein kinase C useful
PT for diagnosis and treatment of cancer and psoriasis.
XX PS Claim 1; Col 15; 54pp; English.
XX CC The present invention describes a method of inhibiting the expression of
CC human protein kinase C (PKC) in cells. The method comprises contacting
CC the cells with an antisense oligonucleotide which has up to 50 nucleotide

CC units. AAX83633 to AAX83720 represent specifically claimed antisense
CC oligonucleotides for use in the method of the invention. The antisense
CC oligonucleotides modulate hybridize to messenger RNA from the PKC gene
CC which results in modulation of expression of the PKC gene. This means
CC they can be used for diagnosis, therapeutic or prophylactic treatment of
CC PKC associated diseases such as cancer and psoriasis, and as research
CC agents. Abnormal proliferative states in tissue from patients suspected
CC of having a hyperproliferative disease e.g. cancer, psoriasis can be
CC diagnosed. Tumours associated with PKC can be distinguished from tumours
CC which are not PKC associated to allow an efficacious treatment regime to
CC be used. The antisense oligonucleotides have specific activity so are
CC able to modulate PKC activity without producing side effects and with
CC greater effectiveness than observed from administration of current
CC agents. AAX83721 to AAX83753 represent other oligonucleotides used in
CC examples from the present invention

SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 11
AAX19156/c
ID AAX19156 standard; DNA; 20 BP.
AC AAX19156;
XX
XX 20-MAR-2003 (revised)
DT 14-MAY-1999 (first entry)
XX
XX Human PKC-beta type II antisense oligonucleotide SEQ ID NO:30.
DE
XX Human; PKC; protein kinase C; diagnosis; antisense oligonucleotide;
KW phosphorothioate linkage; hyperproliferative disease; cancer; psoriasis;
KM tumour; inhibition; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5882927-A.
PN
XX 16-MAR-1999.
PD
XX 07-JUN-1995; 95US-00478178.
PF
XX 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Dean N, Bennett CF;
PI
XX WPI; 1999-214073/18.
DR
XX
XX New synthetic oligonucleotides inhibiting expression of protein kinase C
PT (PKC)-alpha - useful for treating and diagnosing conditions associated
PT with abnormal PKC expression.
XX
XX Example 4; Col 16; 56pp; English.
PS
XX The present invention specifically describes antisense oligonucleotides
CC of up to 50 nucleotides in length which specifically bind human protein
CC kinase C-alpha (PKC-alpha) mRNA. AAX19127 to AAX19247 represent antisense
CC oligonucleotides from the present invention which bind human PKC-alpha, -
CC beta, -gamma, -delta, -epsilon, -zeta and -eta. The antisense
CC oligonucleotides modulate the expression of the PKC gene (i.e. inhibit
CC the PKC gene). The antisense oligonucleotides can be used to diagnose

CC abnormal proliferative states in tissue or other samples from patients
CC suspected of having a hyperproliferative disease e.g cancer or psoriasis.
CC The antisense oligonucleotides can be used to distinguish PKC-associated
CC tumours and to detect and diagnose PKC expression (through the use of 32P
CC labeled antisense oligonucleotides). Radiolabeled antisense
CC oligonucleotides can also be used to perform autoradiography of tissues
CC to determine the localization, distribution and quantitation of PKC
CC expression for research, diagnostic and therapeutic purposes. The use of
CC the antisense oligonucleotides eliminate the side effects associated with
CC prior art methods because it modulates the amount of PKC protein made
CC from the gene rather than inhibiting the enzyme itself. (Updated on 20-
CC MAR-2003 to correct PF field.)

SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 43.6%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 12
AAZ27295/c
ID AAZ27295 standard; DNA; 20 BP.
AC AAZ27295;
XX
XX 01-DEC-1999 (first entry)
DT
XX
XX Human protein kinase C beta antisense oligonucleotide #10.
DE
XX Human; protein kinase C; PKC; diagnosis; antisense oligonucleotide;
KW phosphorothioate; hybridisation; isozyme; target; inflammation;
KM hyperproliferative disorder; psoriasis; tumour; cancer; glioblastoma; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5959096-A.
PN
XX 28-SEP-1999.
PD
XX 07-JUN-1995; 95US-00481066.
PF
XX 16-MAR-1992; 92US-00852852.
PR 09-JUL-1993; 93US-00089996.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Bennett CF, Dean N;
PI
XX WPI; 1999-561076/47.
DR
XX
XX Antisense oligonucleotides useful for treatment of hyperproliferative and
PT inflammatory conditions including psoriasis, tumors and cancer.
PT
XX
XX Claim 1; Col 15; 56pp; English.
PS
XX The present invention describes antisense oligonucleotides up to 50
CC nucleotides in length which specifically bind mRNA encoding human protein
CC kinase C (PKC). AAZ27266 to AAZ27386 represent human PKC antisense
CC oligonucleotides used in the exemplification of the present invention.
CC The antisense oligonucleotides are useful for the treatment of diseases
CC associated with PKC expression, such as hyperproliferative and
CC inflammatory conditions including psoriasis, tumours and cancer
CC (glioblastoma, bladder, breast, colon and lung cancer)

SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 43.6%; Score 17; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
|||
Db 20 CCCGAGTCAAGAGCTA 4

RESULT 13
ABL90883/c

ID ABL90883 standard; DNA; 20 BP.

AC ABL90883;

DT 27-MAY-2002 (first entry)

DE Human protein kinase C-beta (type II) antisense oligonucleotide 1.

KW Human; PKC antisense oligonucleotide; protein kinase C; PKC; PKC-alpha;
KW PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-delta; PKC-epsilon;
KW PKC-zeta; PKC-eta; PKC expression modulation; ss;
KW hyperproliferative condition; tumour; glioblastoma; bladder cancer;
KW breast cancer; colon cancer; lung cancer; inflammatory condition;
KW psoriasis; phosphorothioate backbone.

OS Homo sapiens.

PN US6339066-B1.

PD 15-JAN-2002.

PF 31-MAR-1997; 97US-00829637.

PR 11-JAN-1990; 90US-00463358.

PR 13-AUG-1990; 90US-00566977.

PR 11-JAN-1991; 91WO-US000243.

PR 15-OCT-1991; 91US-00777760.

PR 16-OCT-1991; 91US-00777007.

PR 16-MAR-1992; 92US-00852852.

PR 05-MAY-1993; 93US-00058023.

PR 09-JUL-1993; 93US-00089996.

PR 29-AUG-1994; 94US-00297703.

PR 07-JUN-1995; 95US-00481066.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Dean NM, Cook PD, Hoke G;

PT WPI; 2002-215022/27.

PT New antisense oligonucleotide having nucleoside units which specifically

binds mRNA encoding human protein kinase C isoform, useful for treating

hyperproliferative and inflammatory diseases e.g. psoriasis, tumor and

cancer.

PS Claim 6; Col 44; 77pp; English.

XX The invention comprises antisense oligonucleotides designed to bind mRNA

encoding a human protein kinase C (PKC) isoform (i.e. PKC-alpha, PKC-beta

type I, PKC-beta type II, PKC-gamma, PKC-delta, PKC-epsilon, PKC-zeta,

and PKC-eta). The antisense oligonucleotides of the invention are useful

for modulating the expression of the PKC isoforms. The antisense

oligonucleotides are useful for treating hyperproliferative conditions

(e.g. tumour, glioblastoma, bladder cancer, breast cancer, colon cancer

and lung cancer), and inflammatory conditions (e.g. psoriasis). The

antisense oligonucleotides of the invention are also useful for detection

and diagnosis of PKC expression. The present sequence represents a human

PKC antisense oligonucleotide of the invention. NOTE: The present

sequence contains a phosphorothioate backbone

Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 43.6%; Score 17; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36
|||
Db 20 CCCGAGTCAAGAGCTA 4

RESULT 14
ACH11162/c

ID ACH11162 standard; DNA; 20 BP.

AC ACH11162;

DT 08-OCT-2003 (first entry)

DE Human protein kinase C-beta targeted oligonucleotide #10.

KW Human; ss; antisense; PKC; protein kinase C; hyperproliferation; tumour;
KW inflammation; psoriasis; cancer; non-small cell lung cancer; lung cancer;
KW non-Hodgkin's lymphoma; glioblastoma; bladder cancer; colon cancer;
KW breast cancer; ovarian cancer; pancreatic cancer.

OS Homo sapiens.

PN US6537973-B1.

PD 25-MAR-2003.

PF 18-DEC-2001; 2001US-00025139.

PR 16-MAR-1992; 92US-00852852.

PR 09-JUL-1993; 93US-00089996.

PR 07-JUN-1995; 95US-00478178.

PR 31-MAR-1997; 97US-00829637.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Dean NM, Holmlund JT, Dorr FA;

PT WPI; 2003-531084/50.

PT New pharmaceutical composition, useful for treating cancer, e.g., non-

small cell lung cancer or non-Hodgkin's lymphoma.

PS Example 4; Col 16; 56pp; English.

XX The invention relates to a new pharmaceutical composition comprising: (a)

an oligonucleotide sequence having up to 50 base pairs (bp); and (b)

carboplatin and paclitaxel, cisplatin and gemcitabine, 5-fluorouracil and

leucovorin, or docetaxel. The pharmaceutical composition is useful for

treating diseases associated with protein kinase C such as

hyperproliferative and inflammatory conditions e.g. psoriasis, tumours

and cancer e.g. non-small cell lung cancer, non-Hodgkin's lymphoma,

glioblastoma, bladder cancer, lung cancer, colon cancer, breast cancer,

ovarian cancer and pancreatic cancer. The present sequence represents an

antisense oligonucleotide targeted against protein kinase C

Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 43.6%; Score 17; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAGTCAAGAGCTA 36

|||

Db 20 CCCGAGTCAAGAGCTA 4

RESULT 15

AAF70175

ID AAF70175 standard; DNA; 26 BP.

AC AAF70175;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE Human TNFRSF1B gene promoter fragment 3 PCR primer.
 XX
 KW Human; TNFRSF1B; osteoclastogenesis inhibitory factor;
 KW single nucleotide polymorphism; SNP; osteoclast recruitment;
 KW osteoclast function; osteoporosis; metastatic bone disease;
 KW Paget's disease; rheumatoid arthritis; periodontal bone disease;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 EN WO200104137-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 10-JUL-2000; 2000WO-US018803.
 XX
 PR 09-JUL-1999; 99US-0143020P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
 XX
 DK WPI; 2001-147175/15.
 XX
 PT Human Osteoclastogenesis Inhibitory Factor nucleotides, comprising single
 PT nucleotide polymorphisms, useful for studying e.g. osteoporosis, Paget's
 PT disease and rheumatoid arthritis.
 XX
 PS Example 1B; Page 38; 114pp; English.
 XX
 CC The present sequence is a primer used to isolate polymorphic regions of
 CC the human osteoclastogenesis inhibitory factor (TNFRSF1B).
 CC Polynucleotides comprising one or more of twenty four novel single
 CC nucleotide polymorphisms in the TNFRSF1B gene have been identified.
 CC TNFRSF1B regulate osteoclast recruitment and function. An understanding
 CC of variations in the gene should thus be useful in developing new
 CC therapies for metabolic disorders caused by abnormal osteoclast
 CC recruitment and function such as osteoporosis, metastatic bone disease,
 CC Paget's disease, rheumatoid arthritis and periodontal bone disease
 CC
 SQ Sequence 26 BP; 8 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 43.6%; Score 17; DB 4; Length 26;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 7 TGAATTTTAAACCGAAGTCAAG 31
 |||||
 DB 2 TGAGGTTTCAGAACCGAAGTGAAG 26

Search completed: March 20, 2004, 12:25:12
 Job time : 248 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 08:36:30 ; Search time 195 Seconds

(without alignments)
739.831 Million cell updates/sec

Title: US-09-435-471B-9

Perfect score: 39
Sequence: 1 taactctgaatttttaaacccgaagtcagagctagta 39

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 1466766

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	49.7	50	15	US-10-131-827-5310 Sequence 5310, App
2	18.6	47.7	47	15	US-10-349-143-563 Sequence 563, App
3	17	43.6	20	14	US-10-348-485-30 Sequence 30, Appl
4	16.8	43.1	50	15	US-10-131-827-5650 Sequence 5650, App
5	16	41.0	25	14	US-10-098-263B-1205 Sequence 1205, App
6	16	41.0	47	12	US-10-333-429-87 Sequence 87, Appl
7	15.8	40.5	42	13	US-10-025-367-17 Sequence 17, Appl
8	15.8	40.5	47	15	US-10-349-143-320 Sequence 320, App
9	15.8	40.5	50	15	US-10-131-827-1352 Sequence 1352, App
10	15.8	40.5	50	15	US-10-131-827-2732 Sequence 2732, App
11	15.8	40.5	50	15	US-10-131-827-4948 Sequence 4948, App
12	15.8	40.5	51	14	US-10-287-919-1953 Sequence 1953, App
13	15.8	40.5	60	9	US-09-894-844-132 Sequence 132, App
14	15.8	40.5	60	9	US-09-894-844-133 Sequence 133, App
15	15.8	40.5	60	10	US-09-908-975-13125 Sequence 13125, A

16	15.8	40.5	60	15	US-10-388-902-132 Sequence 132, App
17	15.8	40.5	60	15	US-10-388-902-133 Sequence 133, App
18	15.6	40.0	25	14	US-10-098-263B-19187 Sequence 19187, A
19	15.6	40.0	43	14	US-10-032-585-1924 Sequence 1924, App
20	15.6	40.0	50	14	US-10-286-896-23 Sequence 23, Appl
21	15.4	39.5	60	10	US-09-908-975-11926 Sequence 11926, A
22	15.2	39.0	47	12	US-10-294-934-775 Sequence 775, App
23	15	38.5	42	9	US-09-865-807-21 Sequence 21, Appl
24	15	38.5	42	10	US-09-954-594A-21 Sequence 21, Appl
25	15	38.5	42	10	US-09-974-685-21 Sequence 21, Appl
26	15	38.5	42	14	US-10-197-185-21 Sequence 21, Appl
27	15	38.5	42	15	US-10-387-304-21 Sequence 13, Appl
28	15	38.5	50	15	US-10-164-717-13 Sequence 5393, App
29	15	38.5	60	10	US-09-908-975-5393 Sequence 11986, A
30	15	38.5	60	10	US-09-908-975-11986 Sequence 12989, A
31	15	38.5	60	10	US-09-908-975-14520 Sequence 14520, A
32	15	38.5	60	10	US-09-908-975-21363 Sequence 21363, A
33	15	38.5	25	14	US-10-098-263B-35096 Sequence 35096, A
34	14.8	37.9	43	14	US-10-032-585-806 Sequence 806, App
35	14.8	37.9	43	14	US-10-032-585-1839 Sequence 1839, App
36	14.8	37.9	47	12	US-10-294-934-683 Sequence 683, App
37	14.8	37.9	50	10	US-09-993-346-517 Sequence 517, App
38	14.8	37.9	50	10	US-09-908-975-17283 Sequence 17283, A
39	14.8	37.9	60	10	US-10-098-263B-64316 Sequence 64316, A
40	14.6	37.4	25	14	US-10-098-263B-64316 Sequence 23, Appl
41	14.6	37.4	33	10	US-09-828-455-23 Sequence 24, Appl
42	14.6	37.4	33	10	US-09-828-455-24 Sequence 3372, App
43	14.6	37.4	47	15	US-10-349-143-3372 Sequence 434, App
44	14.6	37.4	50	10	US-09-993-346-434 Sequence 434, App
45	14.6	37.4	50	10	US-09-993-346-434 Sequence 434, App

ALIGNMENTS

RESULT 1
US-10-131-827-5310
; Sequence 5310, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5310
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-5310

Query Match 49.7%; Score 19.4; DB 15; Length 50;
Best Local Similarity 79.3%; Pred. No. 5e+02;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAAGTCAA 30
|||
Db 4 AAGTTGAATTGTCAATCCCAAGTCAA 32

RESULT 2
US-10-349-143-563/C
; Sequence 563, Application US/10349143

Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 563
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-15441-337 : polymorphic base A or C
US-10-349-143-563

Query Match 47.7%; Score 18.6; DB 15; Length 47;
Best Local Similarity 68.6%; Pred. No. 1e+03;
Matches 24; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 TAACTCTGAATTTTAAACCCGAGTCAAGAGCT 35
Db 46 TCACTAAATAATTTTTCACCTTCAAGTCAATAGCT 12

RESULT 3
US-10-348-485-30/c
Sequence 30, Application US/10348485
Publication No. US20030148989A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Holmlund, Jon T.
APPLICANT: Dorf, F. Andrew
TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
FILE REFERENCE: ISIS4954
CURRENT APPLICATION NUMBER: US/10/348,485
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/10/025,139
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 08/829,637
PRIOR FILING DATE: 1997-03-31
PRIOR APPLICATION NUMBER: US 08/478,178
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/089,996
PRIOR FILING DATE: 1993-07-09
PRIOR APPLICATION NUMBER: US 07/852,852
PRIOR FILING DATE: 1992-03-16
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-30

Query Match 43.6%; Score 17; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CCCGAAGTCAAGAGCTA 36
Db 20 CCCGAAGTCAAGAGCTA 4

RESULT 4
US-10-131-827-5650/c
Sequence 5650, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5650
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-5650

Query Match 43.1%; Score 16.8; DB 15; Length 50;
Best Local Similarity 66.7%; Pred. No. 5.2e+03;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 4 CTCTGAATTTTAAACCCGAAGTCAAGAGCTAGTA 39
Db 39 CTCTGATTATTTCGATCCGAGTCTAGTAGGCTA 4

RESULT 5
US-10-098-263B-1205
Sequence 1205, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 1205
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-1205

Query Match 41.0%; Score 16; DB 14; Length 25;
Best Local Similarity 79.2%; Pred. No. 9.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 14 TTAACCCGAAGTCAAGAGCTAG 37
Db 2 TTAATCCGAAGACAGTCTCTCG 25

RESULT 6
US-10-333-429-87/c
Sequence 87, Application US/10333429


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; Publication No. US20040048265A1
; GENERAL INFORMATION:
; APPLICANT: GENSET
; TITLE OF INVENTION: Obesity Associated Biallelic Marker Maps
; FILE REFERENCE: G-083US02PCT
; CURRENT APPLICATION NUMBER: US/10/333,429
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/IB01/01477
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/219,704
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 579
; SOFTWARE: Patent.pm
; SEQ ID NO 87
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-26989-152 : polymorphic base C or T
; US-10-333-429-87

Query Match
Best Local Similarity 41.0%; Score 16; DB 12; Length 47;
Matches 22; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 6 CTGAATTTTAAACCCGAAGTCAAGAGCTAGTA 39
DB 47 CAGAAATTTTAAATCAGGTGTCRCATTAAGTA 14

RESULT 7
; US-10-025-367-17/c
; Sequence 17, Application US/10025367
; Publication No. US20020165186A1
; GENERAL INFORMATION:
; 9118 m2/sr
; APPLICANT: Viacell Biotech GmbH
; TITLE OF INVENTION: Compounds that affect CD83 expression, pharmaceutical
; TITLE OF INVENTION: Compositions comprising said compounds and methods for
; TITLE OF INVENTION: Identifying said compounds
; FILE REFERENCE: 84201
; CURRENT APPLICATION NUMBER: US/10/025,367
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-025-367-17

Query Match
Best Local Similarity 40.5%; Score 15.8; DB 13; Length 42;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 CTCTGAATTTTAAACCCGAAGTCAA 30
DB 28 CTCTGATTTCTTAAACCCGGGTAAA 2

RESULT 8
; US-10-349-143-320
; Sequence 320, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
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; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 320
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-14204-468 : polymorphic base G or T
; US-10-349-143-320

Query Match
Best Local Similarity 40.5%; Score 15.8; DB 15; Length 47;
Matches 20; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 TAACTCTGAATTTTAAACCCGAAGTCA 29
DB 13 TAATCTTAATKTTTAAAGATGTAGTAA 41

RESULT 9
; US-10-131-827-1352
; Sequence 1352, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1352
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-1352

Query Match
Best Local Similarity 40.5%; Score 15.8; DB 15; Length 50;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 AACTCTGAATTTTAAACCCGAAGTCAAGAGCTA 36
DB 8 AAATCTGATTTTGGAAACGAGTATGGAGAGCTA 42

RESULT 10
; US-10-131-827-2732/c
; Sequence 2732, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2732
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-2732

Query Match      40.5%; Score 15.8; DB 15; Length 50;
Best Local Similarity 65.7%; Pred. No. 1.3e+04;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 TAACTCTGAATTTTAAACCCGAAGTCAAGAGCT 35
Db      43 TATGTATTATTATTAGAACTGATGCTCAGAGTT 9

RESULT 11
US-10-131-827-4948
; Sequence 4948, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4948
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-4948

Query Match      40.5%; Score 15.8; DB 15; Length 50;
Best Local Similarity 65.7%; Pred. No. 1.3e+04;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      2 AACTCTGAATTTTAAACCCGAAGTCAAGAGCTA 36
Db      8 AAATCTGATTTTGGAAACGAGTATTGAGAGACTA 42

RESULT 12
US-10-287-919-1953/c
; Sequence 1953, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
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; SEQ ID NO 1953
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1161190)...(1161241)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 2488
; US-10-287-919-1953

Query Match      40.5%; Score 15.8; DB 14; Length 51;
Best Local Similarity 89.5%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AACTCTGAATTTTAAAC 20
Db      32 ATCTCTGATTTTAAAC 14

RESULT 13
US-09-894-844-132
; Sequence 132, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 60
; TYPE: DNA
; ORGANISM: M. tuberculosis
; US-09-894-844-132

Query Match      40.5%; Score 15.8; DB 9; Length 60;
Best Local Similarity 74.1%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      2 AACTCTGAATTTTAAACCCGAAGTC 28
Db      19 AATTGTGAATTCATCAAGCCGTAGTC 45

RESULT 14
US-09-894-844-133
; Sequence 133, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
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```

